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US-09-248-796A-15143
US-09-248-796A-15143
Sequence 15143, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANTILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 EHPRHLIPSLCRQFYHLGWVTGTGGGMSIKYNDEIYIAPSGVQKERMQPEDLFVQDITGK 107
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CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 43331
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; ORGANISM: Drosophila melanogaster
US-09-270-767-43331
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Matches 124; Conservative
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Sequence 32.
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9000, Ap
10152, A
12402, A
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Sequence 15143, A
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18, Appl
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-489-093A-13421
US-09-172-952-32
US-09-172-952-18
US-09-172-952-18
US-09-107-532A-4317
US-09-107-532A-5562
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-09-489-039A-13768
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                                                                                                    OM protein - protein search, using sw model
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1322
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40; Indels

48.1%; Score 636; DB 4; Length 240; 68.9%; Pred. No. 3e-62;

16; Mismatches

81

141

28	85.5	6.5	298	4	-09	Seguence 2717, Ap	
59	84	6.4	462	4	US-09-129-112-15	15,	
30	80.5	6.1	260	m	US-08-081-929-10	10,	
31	80	6.1	399	4	-09	8023	
32	80	6.1	3594	4	US-09-911-842A-4		
33	79.5	6.0	1729	4	US-09-553-690-2	~	
34	78.5	5.9	741	4	US-09-543-681A-8128		
35	77.5	5.9	1497	н	US-08-623-679-7		
36	77.5	5.9	1497	m	US-08-933-774-7	Sequence 7, Appli	
37	77.5	5.9	1497	m	US-09-181-030-7	7	
38	77.5	5.9	1497	m	US-09-534-242-7	7	
39	77.5	5.9	1497	ო	US-09-454-854-7	7	
40	77.5	5.9	1497	m	US-09-164-671-7	7	
41	77.5	5.9	1497	4	US-09-182-113-7	7	
42		5.9	1533	-	-08-623	ο,	
43	77.5	5.9	1533	m	US-08-933-774-9	6	
44	77.5	5.9	1533	m	-09-18	9	
45	77.5	5.9	1533	m	19-534	6	
					ALIGNMENTS		
RESULT 1					•		
တ	0-767-43	331		Ē	79707007		
, Patent No.	No. 670	6703491	TCGCTO!	3	Begarice 13331, Application 03/032/0/8/ Patent No. 6703491		
	GENERAL INFORMATION:	MTION:					
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23 GWAPATGGNMSVRQDDTWCWLSESGRDKGSLTTEDFLQVEI----ATNQAPSGR-KPSAE 77
183 DTCAVIVRRHGIFVWGPTIDKAKIFNEAIDYLMELAIKMYQMGI-PPDCGIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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12.7%; Score 168.5; DB 4;
Best Local Similarity 25.7%; Pred. No. 2.3e-10;
Matches 54; Conservative 33; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 149; DB 4; ilarity 24.7%; Pred. No. 2.7e-08; Conservative 37; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 VLVRRHGVYVWGETWEKAKTMCECYDYLFD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-30160
; Sequence 30160, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
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Matches 47; Conserv
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US-09-489-039A-13421
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; Sequence 461, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
APPLICANT: Gidt, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-54
; TITLE REFERENCE: 15966-54
; CURRENT APPLICATION NUMBER: 06/127,352
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR PILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeeFormatter Version 0.9
; SEQ ID NO 461
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                                                                                                                                                                                                                                                                                                                                                                                                                 ----GYYRYDDMLVVPIIENTPEEKGLKD 175
                                                                                                                                                                                                                                             19 ODKEHPRYLIPELCKOFYHLGWYTGTGGGISLKHGDE----IYIAPSGVQKERIQPEDM 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                         74 FVCDI-NEKDISGPS--PSK----KLKKSQCTPLFMNAYTWRGAGAVIHTHSKAAVMAT
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 RMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGL 229
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                                                                                                                                                                   Length 284;
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37.4%; Score 495; DB 4; Length 244;
Best Local Similarity 45.9%; Pred. No. 1.4e-46;
Matches 107; Conservative 37; Mismatches 69; Indels :
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OTHER INFORMATION: Polypeptide Accession Number YJR024C
                                                                                                                                                                Query Match
41.3%; Score 546.5; DB 4
Best Local Similarity 50.4%; Pred. No. 3.3e-52;
Matches 118; Conservative 29; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                         126 LLFPG-REFKITHQEMIKGIKKCTSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Saccharomyces cerevisiae
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SEQ ID NO 15143
LENGTH: 284
                                                                                   TYPE: PRT
, ORGANISM: Candida albicans
US-09-248-796A-15143
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Sequence 13421, Application US/09489039A

Sequence 13421, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE REPERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PLILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQUENCE: 13421
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
RIOR APPLICATION NUMBER: US 60/094,190
RIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30160
LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 DDVLA-----TDLAGNSLEPGKKPSAETLLHTQLYAWNPAIGAVLHTHSVNATVLSRLVR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 GREFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 GDRLVLQDYELQKAF-----AGVTTHEGQVEVPIFDNDQDIARLASRVQPWLEAHPHCPG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GWVTGTGGGISLKHGDE-IYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 SRRCGAQD-KEHPRYLIPELCKQFYHLGWVTGTGGGISLKHGDE-IYIAPSGVQKERIQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 238;
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US-09-583-110-4749
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                                   98 TPLFMNAYTM-RGAGAVIHTHSKAAVMATLLFPGREFKITHQEMIKGIKKCTSGGYYRYD 156
                                                                                                                                 157 DMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDY 216
                                                                                                                                                                                83 ISGPSPSKKLKKSQCTPLFMNAYTWRG-AGAVIHTHSKAAVM---ATLLFPGREFKITHQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 EMIKGIKKCTS-----GGYYRYDDMLVVPIJENTPEEKGLKDRMAHAMNEYPDSCAVL 191
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Sequence 32, Application US/09172952

Fatent No. 6368793

GENERAL INFORMATION:

APPLICANT: Hoch, James

APPLICANT: Dartois, Veronique

TITLE OF INVENTION: METABOLIC SELECTION METHODS

FILE REFERENCE: 234/191

CURRENT APPLICATION NUMBER: US/09/172,952

CURRENT FILING DATE: 1998-10-14

NUMBER OF SEQ ID NOS: 33

SEQ ID NOS: 33

SEQ ID NO 32

LENGTH: 231
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Patent No. 6368793
GENERAL INFORMATION:
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILLE REFERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FRatSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 238
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Best Local Similarity 28.89
Matches 68; Conservative
                                                                                                                                                                                                                                                                         217 LPDIAVSMKK 226
                                                                                                                                                                                                                                                                                                                                       193 LFECELMRRR 202
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APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE REPERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                    74 SSDTPTHLALYRRYPQIGGIVHTHSRHATIWSQAGLDLPA--WGTTHADYFYGAIPCTRR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 MTVEEINGEYEYQ---TGEVIIKTFEQRGLDPA----QIP---AVLVHSHGPFAWGKD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 KDEVEVAYEKDTGLV--1VEEF-EHRGLNP-----VEVP---GIVVRNHGPFTWGKNPE 183
                                                                                                                                                                                                                                                                                                                                                                                                                150 -----GGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG-- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 CTPLFMNAY-TWRGAGAVIHTHSKAAVMATLLFPGRE---FKITHQEMIKGIKKCTSG-- 150
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                                                                                                                                                                                                      20 GLVTFTWGNVSAV--DETRKLMVIKPSGVEYEVMTADDMVVVEM----ASGKVVEGGKKP
                                                                                                                                                                                                                                                                             95 SQCTPLFMNAY-TMRGAGAVIHTHSKAAVM---ATLLFPGREFKITHQEMIKGIKKCTS-
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                                                                                                                                          39 GWVTGTGGGISLKHGDE----IYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                      40;
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Length 238;
                                                                      78; Indels
ch 10.4%; Score 137; DB 3; Smilarity 30.5%; Pred. No. 7.3e-07; 61; Conservative 21; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
8.09-107-532A-4317
8.5equence 4317, Application US/09107532A
9 Patent No. 6583275
Patent No. GENERAL INPORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4749, Application US/09583110
Patent No. 6699703
BARERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 -- ETWEKAKTMCEC-YDYLF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 AADAVHNAVVLEECAYMGLF 199
Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-583-110-4749
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COMPUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION:
TELEPHONE: (781) 893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 TTKEIKGNY----ELETGKVIVETFLSRGIE-
                 CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SSCTYARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 233 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5562: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 27.89
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
  FILE REFERENCE: 234/191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                    ORGANISM: YiaS-Hi
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US-09-107-532A-5562
                                                                                                                                                                                            US-09-172-952-33
                                                                                                                                                   TYPE: PRT
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ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 DISGPSPSKKLKKSQCTPLFMNAY-TWRGAGAVIHTHSKAAVMATLLFPGRE---FKITH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 ADAFYGKVPCTRQLTKEEVREAYEVHTGN-------VIVETFKERKLDP-----N 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 PRYLIPELCKQFYHLGWVTGTGGGISL--KHGDEIYIAPSGVQKERIQPEDMFVCDINEK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KIMCECYDYLFD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.8%; Score 130; DB 4; Length 241;
Best Local Similarity 26.5%; Pred. No. 4.4e-06;
Matches 63; Conservative 21; Mismatches 74; Indels
                                                           ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-172-952-33
US-09-172-952-33
Sequence 33, Application US/09172952
Patent No. 6368793
GENERAL INFORMATION:
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...241
SEQUENCE DESCRIPTION: SEQ ID NO: 4317:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 EYPDSCAVLVRRHGVYVWGETWEKA----
                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                             COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                               STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277

MATION FOR SEQ ID NO: 4317:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                        STATE: Massachusetts
                 NUMBER OF SEQUENCES: 731
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 QEMIKGIKKCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
                                                                                                       CITY: Waltham
                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-107-532A-4317
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Sequence 5562, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                               94 KSQCTPLFWNAY-TWRGAGAVIHTHSK-AAVMATLLFPGREFKITHQEMIKGIKKCT--- 148
                                                                                                                                                                                                                                                                                     149 ----SGGYYRYDDMLVVPIJENTPBEKGLKDRMAHAMNEYPDSC-AVLVRRHGVYVWGE 202
                                                                                                                                                                                                                                                                                                                                                                                                                             ------PDNIPAVLVHSHGPFAWGK 178
                                                                                                                                                                36 YHLGWVTGTGGGISL--KHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLK
                                                                  Gaps
                                                                  33;
9.8%; Score 129.5; DB 3; Length 231; 27.8%; Pred. No. 4.7e-06; tive 24; Mismatches 73; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
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US-09-583-110-4289
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ORGANISM:
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                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                  78 INEKDISGPSPSKKLKKSQCTPLFMNAY-TMRGAGAVIHTHSKAAVM---ATLLFPGREF 133
                                                                                                                                                                                                                                                                                                                                134 KITHQEMIKGIKKCT-----SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEY 184
                                                                                                                                                                                                                                                                                                                                                                      115 GTTHADTFYGSVPCARFLTQQEIDSG--YEYETGKV--IIETFKERK--IDPLA----I 163
                                                                                                                                                                                                           27 LIPELCKQFYHL-----GWVTGTGGGISLKHGDEIY--IAPSGVQKERIQPEDMFVCD 77
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                185 PDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLP 235
                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                               Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.5%; Score 126; DB 2; Length 242; Best Local Similarity 23.6%; Pred. No. 1.2e-05; Matches 45; Conservative 30; Mismatches 84; Indels
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALDEASSES: FISH & Neave of the Americas STREET: New York STATE: New York STATE: New York STATE: New York CUNTRY: United States of America ZIP: 10020 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BATEM: PC-DOS/MS-DOS SOFTWARE: PATEM: Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/472,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
TITLE OF INVENTION: HEAT SHOCK PROTEIN HSP72 FROM
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
NUMBER OF SEQUENCES: 6
                                                                                                         Query Match 9.6%; Score 127.5; DB 4; Best Local Similarity 26.8%; Pred. No. 8e-06; Matches 62; Conservative 29; Mismatches 97;
               NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...233
SEQUENCE DESCRIPTION: SEQ ID NO: 5562:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08472534
Patent No. 5919620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 424
ATTONENYAGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B10V
TELECOMMUNICATION INFORMATION:
TELEFRAM: 212-596-9090
TELEFRAM: 114-8367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ne
                                                                      US-09-107-532A-5562
PEATURE:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6065, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 NIKGEILEAEGDYCPSSEIK-----MIRCYEEREDVRSVVHAHPPIATGFALAHIPLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 EFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEY-PDSCAV 190
                                                                                                                                                                                                                                         132 EFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEY-PDSCAV 190
                                                                                                                   DINEKDISGPS---PSKKLKKSQCTPLFMNAYTMR-GAGAVIHTHSKAAV-MATLLFPGR 131
                                                                                                                                                                                                                                                                                                   -----VPSTMBVPB------AITPYLPDHDVM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 TYSLIESAIVVGAIPITPFG-----VPSTMEVPE-----AITPYLPDHDVM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
AODKEHPRYLIPELCKOFYHLGWVTGTGGGISLK-HGDEIYIAPSGVQKERIQPEDMFVC 76
                                                                                                                                                      2 SQDEKLIREQICDVCHKMWQLGWVAANDGNVSVRLDEDTILATPTGISKSFITPEKLVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 DINEKDISGPS---PSKKLKKSQCTPLFMNAYTMR-GAGAVIHTHSKAAV-MATLLFPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AQDKEHPRYLIPELCKQFYHLGWVTGTGGGISLK-HGDEIYIAPSGVQKERIQPEDMFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.5%; Score 126; DB 4; Length 242; Best Local Similarity 23.6%; Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: US 60/007,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
SEQ ID NO 4289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4289, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                116 TYSLIESAIVVĠAIPITPFĠ---
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                                                                                                                                                                                                                                                                                                                                                                                                                            157 LLENHGALTVG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 LVRRHGVYVWG 201
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US-09-134-000C-6065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08926842B

Sequence 21, Application US/08926842B

Patent No. 6330807

GENERAL INFORMATION:

APPLICANT: Sa-No.

APPLICANT: Sa-No.

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                               29 LGLVKLTWGNVSEINRSLGIIVIKPSGVKYQEMTKEQMVVTDLKGQLLE----TNALKPS 84
                                                                                                                                                                                                                                                                                                                                                                 38 LGWVTGTGGGIS--LKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 -----LSESEIKENYEEFTG-KVIVETFHEQELDPLAVPGVLVYGHGPFTWGMTPEKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 YYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCA----ULVRRHGVYVWGETWEKA 207
                                                                                                                                                                                                                                                                                                                    81; Indels 23; Gaps
                                                                                                                                                                                                                                                                   Query Match 9.5%; Score 125.5; DB 4; Length 241; Best Local Similarity 31.8%; Pred. No. 1.4e-05; Matches 57; Conservative 18; Mismatches 81; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/926,842B

FILING DATE: 10-SEP-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esg., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-089 N
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SSOFTWARE: PALENTIN VERSION 3.1
SSOFTWARE: PALENTIN VERSION 3.1
LENGTH: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium
                                                                                                                                                                      TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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linear
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ORIGINAL SOURCE
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                                                                                                                                                                                                                      US-09-134-000C-6065
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99 PLFWNAY-TMRGAGAVIHTHSK-AAVMATLLFPGREFKITHQEMIKGIKKCTS----- 149
                                                                                                                                                                                                     78 PTHRLLYQAPPTIGGIVHTHSRHATIWAQAGQPIPATGTTHADYFYGTIPCTRKMTEAEI 137
                                                                                        41 VTGTGGGISL--KHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCT 98
                                                                                                                               22 VTLTWGNVSAVDRERGVLVIKPSGVDYSVMTADDMVVVSLE----SGEVVEGHKKPSSDT 77
                                                                                                                                                                                                                                                                                           150 GGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKA 207
8.8%; Score 116.5; DB 3; Length 240; 27.0%; Pred. No. 0.00014; ive 20; Mismatches 83; Indels 27.
                                            48; Conservative
             Best Local Similarity
Matches 48: Conserv
  Query Match
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Search completed: February 1, 2005, 14:30:59 Job time: 42 secs